

28758  
SEQUENCE LISTING

<110> Gertler, Arieh  
Krishna, Radha G.

<120> LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO

<130> 28758.1

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 630

<212> DNA

<213> human leptin receptor binding domain

<220>

<221> CDS

<222> (1)..(630)

<220>

<221> misc\_feature

<222> (6)..(6)

<223> n is a, c, g, or t

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48

tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt  
Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu  
20 25 30

96

gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt  
Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys  
35 40 45

144

tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat  
Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr  
50 55 60

192

ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta  
Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu  
65 70 75 80

240

tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca  
Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser  
85 90 95

288

ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca  
Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro  
100 105 110

336

ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta  
Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu  
115 120 125

384

ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa  
Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln

432

130	135	140	28758
ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met			
145	150	155	480
tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro			
165		170	528
gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp			
180		185	576
gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val			
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atg gat			
Met	Asp		630
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Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu  
20 25 30

Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys  
35 40 45

Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr  
50 55 60

Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu  
65 70 75 80

Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser  
85 90 95

Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro  
100 105 110

Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu  
115 120 125

Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln  
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130

135

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140

Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met  
145 150 155 160

Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro  
165 170 175

Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp  
180 185 190

Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val  
195 200 205

Met Asp  
210

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<220>  
<221> misc\_feature  
<222> (11)..(11)  
<223> Xaa can be any naturally occurring amino acid

<400> 5

Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu  
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<213> Consensus

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 <223> xaa can be any naturally occurring amino acid

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Trp Ser Xaa Trp Ser  
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 <222> (1)..(627)

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tta	act	aaa	atg	act	tgc	aga	tgg	tct	gca	aac	cca	aac	gca	ttg	ctc	96
Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Ala	Asn	Pro	Asn	Ala	Leu	Leu	
20			25										30			

ttg	ggg	agt	tcc	ttg	cag	tta	aga	tac	cac	agg	agc	aaa	att	tat	tgt	144
Leu	Gly	Ser	Ser	Leu	Gln	Leu	Arg	Tyr	His	Arg	Ser	Lys	Ile	Tyr	Cys	
35				40								45				

tct	aac	ttt	cca	agt	act	cct	cca	gaa	tca	gag	gtg	aaa	gaa	tgc	cat	192
Ser	Asn	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Ser	Glu	Val	Lys	Glu	Cys	His	
50			55								60					

ttc	cag	agg	aat	cat	tct	tat	gag	tgc	aca	ttt	cag	cct	gtt	ttt	ctt	240
Phe	Gln	Arg	Asn	His	Ser	Tyr	Glu	Cys	Thr	Phe	Gln	Pro	Val	Phe	Leu	
65		70					75						80			

tta	tct	gga	tat	acc	atg	tgg	att	gag	ctt	aag	cac	tcg	ctg	gga	aca	288
Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Glu	Leu	Lys	His	Ser	Leu	Gly	Thr	
85			90										95			

ctt	gaa	tcc	tca	cca	act	tgt	gtc	gtt	cca	gca	gat	gtg	gtg	aag	cca	336
Leu	Glu	Ser	Ser	Pro	Thr	Cys	Val	Val	Pro	Ala	Asp	Val	Val	Lys	Pro	
100			105									110				

ctg	cct	ccc	tcc	aac	att	aaa	gca	gag	atc	acc	aga	aac	gat	ggg	ctg	384
Leu	Pro	Pro	Ser	Asn	Ile	Lys	Ala	Glu	Ile	Thr	Arg	Asn	Asp	Gly	Leu	
115			120									125				

ctg	aac	gtg	agc	tgg	aca	aac	ccc	gtg	ttt	aca	aat	gat	gac	ctt	aag	432
Leu	Asn	Val	Ser	Trp	Thr	Asn	Pro	Val	Phe	Thr	Asn	Asp	Asp	Leu	Lys	
130			135									140				

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ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg	480
Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu	
145 150 155 160	
tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa	528
Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln	
165 170 175	
ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc	576
Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly	
180 185 190	
tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa	624
Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys	
195 200 205	
gat	627
Asp	

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Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys  
35 40 45

Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His  
50 55 60

Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu  
65 70 75 80

Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr  
85 90 95

Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro  
100 105 110

Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu  
115 120 125

Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys  
130 135 140

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Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu  
145 150 155 160

Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln  
165 170 175

Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly  
180 185 190

Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys  
195 200 205

Asp